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Selten, G. C. M., Veenstra, A. E., van Gorcom, R. F. M., & van den Hondel, C. A. M. J. J. (1993) Cloning, characterization and overexpression of the phytase-encoding gene (phyA) of *Aspergillus niger*. *Gene* 127, 87-94; from aa 27; SEQ ID NO: 5]; phyA from *Aspergillus fumigatus* ATCC 13073 (Pasamontes, L., Haiker, M., Wyss, M., Tessier, M. & van Loon, A. P. G. M. (1997) Cloning, purification and characterization of a heat stable phytase from the fungus *Aspergillus fumigatus*, *Appl. Environ. Microbiol.* 63, 1696-1700; from aa 25; SEQ ID NO: 6]; phyA from *A. fumigatus* ATCC 32722 (EP 897985); from aa 27; SEQ ID NO: 7); phyA from *A. fumigatus* ATCC 58128 (EP 897985); from aa 27; SEQ ID NO: 8); phyA from *A. fumigatus* ATCC 26906 (EP 897985); from aa 27; SEQ ID NO: 9); phyA from *A. fumigatus* ATCC 32239 (EP 897985); from aa 30; SEQ ID NO: 10; phyA from *Emericella nidulans* [Pasamontes, L., Haiker, M., Henriquez-Huecas, M., Mitchell, D. B. & van Loon, A. P. G. M. (1997a). Cloning of the phytases from *Emericella nidulans* and the thermophilic fungus *Talaromyces thermophilus*. *Biochim. Biophys. Acta* 1353, 217-223; from aa 25; SEQ ID NO: 11]; phyA from *Talaromyces thermophilus* (Pasamontes et al., 1997a; from aa 24; SEQ ID NO: 12); and phyA from *Myceliophthora thermophila* (Mitchell et al., 1997; from aa 19; SEQ ID NO: 13). The alignment was calculated using the program PILEUP. The location of the gaps was refined by hand. Capitalized amino acid residues in the alignment at a given position belong to the amino acid coalition that establish the consensus residue. In bold, beneath the calculated consensus sequence (SEQ ID NO: 98), the amino acid sequence of the finally constructed consensus phytase (Fcp) is shown (SEQ ID NO: 14). The gaps in the calculated consensus sequence were filled by hand according to principals stated in Example 1.

Concluded

Please replace the paragraph from page ²⁰~~17~~, line 27 – page ²¹~~18~~, line 15 with:

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Figure 5: DNA and amino acid sequence of consensus phytase-10 (SEQ ID NO: 25, and SEQ ID NO: 26, respectively). The amino acid sequence of the mature consensus phytase-10 is shown in SEQ ID NO:24. The sequence of the oligonucleotides that were used to assemble the gene are in bold letters. The names of the respective oligonucleotides and the amino acids that differ relative to consensus phytase-1 are underlined. The fcp10 gene was assembled from the following oligonucleotides: CP-1, CP-2, CP-3.10, CP-4.10, CP-5.10, CP-6, CP-7.10, CP-8.10, CP-9.10, CP-10.10, CP-11.10, CP-12.10, CP-13.10, CP-14.10, CP-15.10, CP-16.10, CP-17.10, CP18.10, CP-19.10, CP-20.10, CP-21.10, and CP-22.10. The newly synthesized oligonucleotides are additionally marked by the number 10. The phytase contains the following 32 exchanges

B2 relative to consensus phytase-1: Y54F, E58A, D69K, D70G, A94K, N134Q, I158V, S187A, Q188N, D197N, S204A, T214L, D220E, L234V, A238P, D246H, T251N, Y259N, E267D, E277Q, A283D, R291I, A320V, R329H, S364T, I366V, A379K, S396A, G404A, Q415E, A437G, A463E. The underlined mutations revealed a stabilizing effect on consensus phytase-1 when tested as single mutations in consensus phytase-1.

Please replace the paragraphs on page 27, line 11-25 with:

B3 Figure 22: DNA and amino acid sequence of consensus phytase-3-thermo[11]-Q50T (SEQ ID NOS:90-91).

Figure 23: DNA and amino acid sequence of consensus phytase-3-thermo[11]-Q50T-K91A (SEQ ID NOS:92-93).

Figure 24: DNA and amino acid sequence of consensus phytase-10-thermo[5]-Q50T (SEQ ID NOS:94-95).

Figure 25: DNA and amino acid sequence of consensus phytase-10-thermo[5]-Q50T-K91A (SEQ ID NOS:96-97).

✓ Please insert the attached Sequence Listing (pages 1-105) at the end of the specification.